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 134 lYArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150  
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 151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGlyAlaProle 167  
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seq\_name: gb\_fo:MM088325

seq\_documentation block:

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 DEFINITION Mus musculus suppressor of cytokine signalling-1 (SOCS-1) mRNA,  
 complete cds.  
 ACCESSION U88325  
 VERSION U88325  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,  
 and Hilton, D.J.  
 1 (bases 1 to 1185)  
 A family of cytokine-inducible inhibitors of signalling

TITLE  
 JOURNAL Nature 387 (6636), 917-921 (1997)  
 MEDLINE 97345633  
 REFERENCE 2 (bases 1 to 1185)  
 AUTHORS Starr, R., Willison, T.A., Viney, E.M., Murray, L.J.L., Rayner, J.R.,  
 Jenkins, B.J., Gonda, T.J., Alexander, W.S., Metcalf, D., Nicola, N.A.,  
 and Hilton, D.J.  
 Direct Submision  
 Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza  
 Hall Institute of Medical Research, PO Royal Melbourne Hospital,  
 VIC 3050, Australia

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 117 rValysMetAlaSerGlyProThrSerIleArgValHisPheGlnAla 134  
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seq\_documentation\_block: 1193 bp mRNA ROD 10-AUG-1999  
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 complete cds.  
 ACCESSION AF120490  
 VERSION AF120490.1 GI:4581880  
 KEYWORDS  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
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 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 1193)  
 De Sepulveda, P., Okkenhaug, K., La Rose, J., Hawley, R.G., Dubreuil, P.  
 and Rottebel, R. Socs1 binds to multiple signalling proteins and suppresses steel  
 factor-dependent proliferation  
 EMBO J. 18 (4), 904-915 (1999)  
 99146908  
 2 (bases 1 to 1193)  
 De Sepulveda, P. and Rottebel, R.  
 Direct Submission  
 Submitted (15-JAN-1999) Experimental Therapeutics, Ontario Cancer  
 Institute, 610 University Avenue, Toronto, ON M5G 2M9, Canada  
 JOURNAL  
 TITLE Location/Qualifiers  
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 ORIGIN

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 Ratio: 5.222 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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seq\_documentation\_block:  
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 DEFINITION Mus musculus mRNA for stat-induced stat inhibitor-1, complete cds.  
 ACCESSION AB000710  
 VERSION AB000710.1 GI:2274773  
 KEYWORDS stat-induced stat inhibitor-1; SSI-1.  
 SOURCE Mus musculus cDNA to mRNA, clone\_1lb:thymus cDNA.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 909)  
 Kishimoto, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-1997) to the DDBJ/EMBL/GenBank databases.  
 Tadamoto, K., Kishimoto, T., Yoshizaki, K., Akira, S. and Kishimoto, T.  
 2-2, Suita 565, Japan (E-mail: matsunot@med3.med.osaka-u.ac.jp,  
 Tel: +81-6-879-3831, Fax: +81-6-879-3839)  
 2 (bases 1 to 909)  
 Naka, T., Narazaki, M., Hirata, M., Tomoshige, M., Minamoto, S.,  
 Nishimoto, N., Kajita, T., Yoshizaki, K., Akira, S. and Kishimoto, T.  
 TITLE Structure and function of a novel STATs-induced inhibitor of STATs  
 JOURNAL function-1 (SIIS-1)  
 REFERENCE Unpublished (1997)  
 AUTHORS Naka, T., Narazaki, M., Hirata, M., Matsumoto, T., Minamoto, S.,  
 Akira, S., Nishimoto, N., Kajita, T., Taga, T., Yoshizaki, K., Akira, S.  
 and Kishimoto, T.  
 TITLE Structure and function of a new STAT-induced STAT inhibitor  
 JOURNAL Nature 387 (6636), 924-929 (1997)  
 MEDLINE 97345635

## FEATURES

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Location/Qualifiers

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## ORIGIN

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Ratio: 5.189

Percent Similarity: 100.000

Length: 212

Gaps: 0

Percent Identity: 99.057

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seq\_name: gb:AB000677

seq\_documentation\_block:

LOCUS AB000677 1056 bp mRNA ROD 22-JUL-1997

DEFINITION Mus musculus mRNA for JAB, complete cds.

ACCESSION AB000677

VERSION AB000677.1 GI:2274771

## KEYWORDS

JAB.

## SOURCE

Mus musculus

## ORGANISM

Mus musculus

## REFERENCE

Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Yoshimura, A.

## TITLE

Submitted (24-JAN-1997) to the DDBJ/EMBL/Genbank databases. Akhiko Yoshimura, Kurume university, Institute of Life Science; 2432-3 Akawa-machi, Kurume 839, Japan (Tel:0942-37-6313, Fax:0942-31-5212)

## JOURNAL

2 (sites)

## REFERENCE

Yoshimura, A.

## TITLE

Cloning of a novel JAK kinase inhibitory SH2 protein

## JOURNAL

3 (sites)

## REFERENCE

Endo, T.A., Masuhara, M., Yokouchi, M., Suzuki, R., Sakamoto, H., Mitsui, K., Matsumoto, A., Tanimura, S., Ohtsubo, M., Misawa, H., Miyazaki, T., Leonor, N., Taniguchi, T., Fujita, T., Kanakura, Y., Komiya, S., and Yoshimura, A.

## TITLE

A new protein containing an SH2 domain that inhibits JAK kinases

## JOURNAL

Nature 387 (6636), 921-924 (1997)

## MEDLINE

97345634

## FEATURES

Location/Qualifiers

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Quality: 1100.00

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## Percent Similarity:

100.000

## Length:

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## Gaps:

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## Percent Identity:

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REFERENCE	JOURNAL
AUTHORS	Submitted (30-MAY-1996) Schluter G., Institut fuer Humangenetik, Universitaet Goettingen, Gosslerstr.12d, Goettingen, germany, 37073 4 (bases 1 to 13812)
TITLE	Schluter,G., Celik,A., Oyata,R., Schlicker,M., Hofferbert,S., Schlung,A., Adham,I.M. and Engel,W. Sequence analysis of the conserved protamine gene cluster shows that it contains a fourth expressed gene
JOURNAL	Mol. Reprod. Dev. 43 (1), 1-6 (1996)
MEDLINE	96341725
COMMENT	On Jun 5, 1996 this sequence version replaced gi:886891. Related sequences: x07625, x07626, M60254.
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seq_documentation_block:
LOCUS BTPRMTNP2 13187 bp DNA ROD 11-DEC-1996
DEFINITION R.norvegicus PRM1, PRM2, PRM3 and TNP2 genes.
ACCESSION Z46939.1 GI:1359527
VERSION Z46939.1 GI:1359527
KEYWORDS PRM1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition
protein 2.

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SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 13187)
AUTHORS Schluter,G., Celik,A., Obata,R., Schlicker,M., Hofferbert,S.,
Schlung,A., Adham,I.M., and Engel,W.
TITLE Sequence analysis of the conserved protamine gene cluster shows
that it contains a fourth expressed gene
JOURNAL Mol. Reprod. Dev. 43 (1), 1-6 (1996)
MEDLINE 96341725
REFERENCE 2 (bases 1 to 13187)
AUTHORS Schluter,G.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1994) Schluter G., Institut fuer Humangenetik,
Universitaet Goettingen, Gosslerstr. 12d, Goettingen, FGR, 37073
REMARK 3 (bases 1 to 13187)
AUTHORS Schluter,G.
TITLE Revised by [3]
JOURNAL Submitted (30-MAY-1996) Schluter G., Institut fuer Humangenetik,
Universitaet Goettingen, Gosslerstr. 12d, Goettingen, FGR, 37073
REFERENCE 4 (bases 1 to 13187)
AUTHORS Schluter,G., Celik,A., Obata,R., Schlicker,M., Hofferbert,S.,
Schlung,A., Adham,I.M., and Engel,W.
TITLE Sequence analysis of the conserved protamine gene cluster shows
that it contains a fourth expressed gene
JOURNAL Unpublished
COMMENT On Jun 5, 1996 this sequence version replaced gi:886853.
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DEFINITION Homo sapiens suppressor of cytokine signalling-1 SOCS-1 gene,
complete cds.
ACCESSION AF132440
VERSION AF132440.1 GI:4680638
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 908)
Yandava,C.N., Pillari,A. and Drazen,J.M.
JOURNAL Radiation hybrid and cytogenetic mapping of SOCS1 and SOCS2 to
MEDLINE Genomics 61 (1), 108-111 (1999)
99443878
REFERENCE 2 (bases 1 to 908)
Yandava,C.N., Pillari,A. and Drazen,J.M.
JOURNAL Direct Submission
TITLE Submitted (01-MAR-1999) Pulmonary and Critical Care Medicine,
Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115,
USA
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DEFINITION Homo sapiens mRNA for STAT Induced STAT Inhibitor-1, complete cds.
ACCESSION AB005043
VERSION AB005043.1 GI:2443364
KEYWORDS STAT induced STAT inhibitor-1.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1082)
REFERENCE
AUTHORS Minamoto,S.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1997) to the DDBJ/EMBL/GenBank databases. Seiji
Minamoto, Osaka University, Internal Medicine III; Yamadaoka 2-2,
Suta, Osaka 565, Japan (E-mail:minamoto@med3.med.osaka-u.ac.jp,
Tel:06-879-3833, Fax:06-879-3839)
2 (sites)
REFERENCE
AUTHORS Minamoto,S., Ikegami,K., Ueno,K., Narazaki,M., Naka,T.,
Yamamoto,H., Matsumoto,T., Saito,H., Hosoe,S. and Kishimoto,T.
TITLE Cloning and functional analysis of new members of STAT Induced STAT
Inhibitor (SSI) family: SSI-2 and SSI-3
JOURNAL Biochem. Biophys. Res. Comm. 237, 79-83 (1997)

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DEFINITION Human suppressor of cytokine signalling-1 (SOCS-1) mRNA, complete cds.
ACCESSION U88326
VERSION U88326.1 GI:2245383
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ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A. and Hilton,D.J.
TITLE A family of cytokine-inducible inhibitors of signalling
JOURNAL Nature 387 (6636), 917-921 (1997)
MEDLINE 97345633
REFERENCE 2 (bases 1 to 1094)
AUTHORS Starr,R., Willison,T.A., Viney,E.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A. and Hilton,D.J.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, VIC 3050, Australia
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JOURNAL

TITLE

AUTHORS

REFERENCE

ORGANISM

SOURCE

VERSION

ACCESSION

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18-NOV-1997

PRI

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AB000734

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AB000734

GI:2627028

AB000734.1 GI:2627028

TIP3; TIP3.

Homo sapiens blood B-lymphocytes cDNA to mRNA.

Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 1216)

Mano,H.

Submitted (27-JAN-1997) to the DDBJ/EMBL/GenBank databases.

Hiroyuki Mano, Jichi Medical School, Department of Molecular Biology; 3311-1 Yakushiji, Minamikawachi-Machi, Kawachi-gun, Tochigi 329-04, Japan (E-mail: hmanoe@jichi.ac.jp, Tel:0285-44-2111(ex.3482), Fax:0285-44-8675)

2 (sites)

Ohya,K.I., Kajiyaya,S., Yamashita,Y., Miyamoto,A., Hatake,R., Miura,Y., Ikeda,Y., Shimada,K., Ozawa,M. and Mano,H.

SCCS-1/JMB/SST-1 can bind to and suppress Tec protein-tyrosine kinase

J. Biol. Chem. 272 (43), 27178-27182 (1997)

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502 CGTAAGAATGGCTCTGGGACCGACGAGATCGGCTGACTTTACAGGGCG 551
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134 lyaArgPheHisLeuAspGlySerArgGlnThrPheAspCysLeuPheGln 150
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552 GCCGCTTACCTGATGGAGCGCGCGAGAGCTTCGACTGCTCTTCTGAG 601

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151 LeuLeuGlnHisTyrValAlaAlaProArgArgMetLeuGlnValaProle 167  
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 602 CTGCTGAGCAGCTACGCGCGCGCGCGCGCTGCGCGCGCGCT 651  
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 167 uArgGlnArgArgValaArgProLeuGlnGluLeuCysArgGlnArgIleVal 184  
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 652 GCGGACAGCGCGCGCTGCGCGCTGAGAGAGCTGTGCGCGCGCGAGCTGCG 701  
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 184 alAlaAlaValaGlyArgGlnAsnLeuAlaArgIleProLeuAsnProVal 200  
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 702 TGGCCACCGTGGCGCGCGAGACCTGCTGCACTCCCGCAACCGCGCTG 751  
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 201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212  
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 752 CTCGCGCAGCTACCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787

seq\_name: gb-p4:AC002286

## seq\_documentation\_block:

LOCUS AC002286 12589 bp DNA PRI 23-NOV-1999  
 DEFINITION Homo sapiens Chromosome 16p13.13 cosmid clone 356d7 from the Los  
 Alamos Chromosome 16 specific Supercos cosmid library complete  
 genomic sequence, complete sequence.

ACCESSION AC002286  
 VERSION AC002286.1 GI:2160310  
 KEYWORDS HTG.

## SOURCE

ORGANISM human.

Homosapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

AUTHORS Kramer,J.A., Adams,M.D., Singh,G.B., Doggett,N.A. and Krawetz,S.A.  
 TITLE Extended analysis of the region encompassing the PRM1-->PRM2-->TNP2  
 domain: genomic organization, evolution and gene identification  
 J. Exp. Zool. 282 (1-2), 245-253 (1998)

## JOURNAL

MEDLINE 98390623

AUTHORS

2 (bases 1 to 12589)  
 Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R.,  
 Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L.,  
 Deslattes,Mays,A., Cao,X., Xu,R.X., Kang,H.L., Mitchell,S.,  
 Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.  
 Genome duplications and other features in 12 Mb of DNA sequence  
 from human chromosome 16p and 16q  
 Genomics 60 (3), 295-308 (1999)

## JOURNAL

MEDLINE 99425270

AUTHORS

3 (bases 1 to 12589)  
 Adams,M.D.  
 Direct Submission  
 Submitted (04-JUN-1997) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA

## JOURNAL

MEDLINE

AUTHORS

4 (bases 1 to 12589)  
 Venter,J.C., Kramer,J.A. and Doggett,N.A.  
 Direct Submission  
 Submitted (28-AUG-1997) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA  
 Address all correspondence to:

## COMMENT

Mark Adams  
 The Institute for Genomic Research  
 9712 Medical Center Dr,  
 Rockville, MD 20850,  
 USA e-mail address: mdamas@tigr.org. The cosmid location is on  
 chromosome 16p13.13. The orientation of the sequence is from SP6  
 end to T7 end. Genes were identified by a combination of five  
 methods including: XGAP (available by anonymous ftp from  
 arthur.epm.ornl.gov), GeneFinder (Phil Green, University of  
 Washington), Genscan (Chris Burge,  
 http://genomic.stanford.edu/~chris/GENSCANW.html) searches of the  
 complete sequence against a peptide database, and the EST database  
 at TIGR (http://www.tigr.org/cdb/at.html). A gene with homology  
 to another protein is annotated as the isoform of that protein.  
 Genes without peptide homology having spliced EST hits are termed  
 'unknown protein'. Genes encoding tRNAs are predicted by

FEATURES tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
Location/Qualifiers

source

1. .12589  
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/db\_xref="taxon:9606"  
/chromosome="16"  
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repeat\_region /rpt\_family="AluSx"  
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repeat\_region /rpt\_family="MIR"  
repeat\_region 9021. .9331  
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repeat\_region complement(12203. .12589)  
misc\_feature /note="has high homology to Human nuclear ribonucleoprotein particle (hnRNP) C protein"  
evidence=not-experimental

BASE COUNT 3067 a 3233 c 3221 g 3068 t  
ORIGIN

alignment\_scores:

Quality: 1053.50 Length: 212  
Ratio: 5.041 Gaps: 1  
Percent Similarity: 98.585 Percent Identity: 95.283

alignment\_block:  
US-08-962-560A-4 x AC002286 ..

Align seg 1/1 to: AC002286 from: 1 to: 12589

1 MetValAlaArgAsnGlnValAlaAlaAspAsnAlaIleSerProAlaAl 17  
|||||.....  
287 ATGTGAGCACAACACAGGTGGACCCGACAAATGACGCTCCACAGCAGC 336  
|||||.....  
17 aglProArgArgArgSerGluProSerSerSerSerSerSerSer 34  
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337 AGAGCCCCGAGCGGGCGGAGAACCT...TCCTCCTCCTCCTCCTCCTGC 383  
|||||.....  
34 roAlaAlaProValArgProArgProCysProAlaValProAlaProAla 50  
|||||.....  
384 CCGGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 433  
|||||.....  
51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArgAr 67  
|||||.....  
434 CCGGCGACAGCAGCACTCCGACATTCGCTTCGACGCGCATTAACGGCG 483  
|||||.....  
67 gileThrArgThrSerAlaLeuAspAlaCysGlyPheTyrTrpGly 84  
|||||.....  
484 CATCAGCGCGCCAGCGCGCTCTGAGCGCTGCGGATTTACTAGGGGCG 533  
|||||.....  
84 roLeuSerValHisGlyAlaHisGluArgLeuAlaGluProValGly 100  
|||||.....  
534 CCGTAGGCTGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583  
|||||.....  
101 ThrPheLeuValArgAspSerArgGlnArgAsnCysPhePheAlaLeu 117  
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584 ACCCTCTCTGTCGCGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCT 633  
|||||.....  
117 rValHisMetAlaSerGlyProThrSerIleArgValHisPheGlnAla 134  
|||||.....  
634 CGTAGAGTGGCTCGGAGCCAGCAGCATCGCGTGCACATTCAGGCGCG 683  
|||||.....  
134 lYArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheGlu 150  
|||||.....  
684 GCCGCTTCACCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGAG 733  
|||||.....  
151 LeuLeuGluHisTyrValAlaAlaProArgArgMetLeuGluAlaProle 167  
|||||.....  
734 CTGCTGGAGCAGCTACGTGGCGCGCGCGCGCGCATGCTGGGGCGCGCT 783  
|||||.....  
167 uArgGlnArgArgValArgProLeuGlnGluLeuCysArgGlnArgIleV 184  
|||||.....  
784 GCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCATCG 833  
|||||.....  
184 alAlaAlaValAlaGlyArgGluAsnLeuAlaArgIleProLeuAspProVal 200  
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834 TGCGCCAGCTGGCGCGCGAGAACCTGCTGCATCCCTCAACCCCGCTC 883  
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seq\_name: gb.htg1:HSAC002047

seq\_documentation\_block: 25417 bp DNA HTG 01-MAY-1997  
LOCUS HSAC002047 25417 bp DNA HTG 01-MAY-1997  
DEFINITION Homo sapiens clone Protamine16, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 2  
unsorted pieces.  
ACCESSION AC002047  
VERSION AC002047.1 GI:2062143  
KEYWORDS HTG; HTGS\_PHASeI.  
SOURCE human.



\* 29281 175950: contigs of 146670 bp in length.  
Location/Qualifiers

FEATURES  
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/db\_xref="taxon:9606"  
/clone="396B14"  
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BASE COUNT 44159 a 44199 c 45076 g 42509 t 7 others  
ORIGIN

## alignment\_scores:

Quality: 1053.50 Length: 212  
Ratio: 5.041 Gaps: 1  
Percent Similarity: 98.585 Percent Identity: 95.283

alignment\_block:  
US-08-962-560a-4 x AC007220 ..

Align seg 1/1 to: AC007220 from: 1 to: 175950

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17 agluproargargargsergluproserserserserserserserp 34
|||||...|||||
5913 AGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5959
34 rolaalaprovalargproargproargproalaproalaproal 50
|||||...|||||
5960 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6009
51 ProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 67
|||||...|||||
6010 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6059
67 glierhargthrseralaleuaspalacysglyphetrtgylp 84
|||||...|||||
6060 CACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6109
84 robuservahisglyalalhisgluargpuearglagluprovalgly 100
|||||...|||||
6110 CCTTGACGTGCACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6159
101 ThrPheLeuValArgAspSerArgGlnArgAsnGlyPhePheAlaLeu 117
|||||...|||||
6160 ACCTTCCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6209
117 rValysMetAlaSerGlyProThrSerIleArgValHisPheGlnAla 134
|||||...|||||
6210 CGGAGAGATGGCTCGGAGCCGAGCAGCATCCGCTGCACTTTCAGGCG 6259
134 lYArgPheHisLeuAspGlySerArgGlnThrPheAspCysLeuPheGlu 150
|||||...|||||
6260 GCCGCTTTCACCTGATGGCAGCGCGAGAGCTTCGACTGCTCTTCGAG 6309
151 LeuLeuGlnHisTyrValAlaAlaProArgArgMetLeuGlyAlaPro 167
|||||...|||||
6310 CTGCTGAGACACTAGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 6359
167 uArgGlnArgValArgProLeuGlnLeuGlyArgGlnArgGlnArg 184
|||||...|||||
6360 GGGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6409
184 aAlaAlaValGlyArgGlnAsnLeuAlaArgIleProLeuAsnProval 200
|||||...|||||
6410 TGGCCACCGTGGCGCGGAGAACCTTGCTGCAATCCCTCAACCCCGCT 6459
201 LeuArgAspTyrLeuSerSerPheProPheGlnIle 212
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seq\_name: gb\_prl:AB000676

seq\_documentation\_block:

LOCUS AB000676 1030 bp mRNA PRI 22-JUL-1997  
DEFINITION Homo sapiens mRNA for JAB, partial cds.  
ACCESSION AB000676  
VERSION AB000676.1 GI:2274769  
KEYWORDS JAB.  
SOURCE Homo sapiens cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Hominoidea; Homo.

## REFERENCE

1 (bases 1 to 1030)  
Yoshimura, A.  
Direct Submission  
Submitted (24-JAN-1997) to the DDBJ/EMBL/GenBank databases. Akhiko  
Yoshimura, Kurume university, Institute of Life Science; 2432-3  
Aikawa-machi, Kurume 839, Japan (Tel:0942-37-6313,  
Fax:0942-31-5212)

## REFERENCE

2 (sites)  
Yoshimura, A.  
Cloning of a novel JAK kinase inhibitory SH2 protein  
Unpublished (1997)

## AUTHORS

Endo, T.A., Masuhara, M., Yokouchi, M., Suzuki, R., Sakamoto, H.,  
Mitsui, K., Matsumoto, A., Tanimura, S., Ohtsubo, M., Misawa, H.,  
Miyazaki, T., Leonor, N., Taniguchi, T., Fujita, T., Kanakura, Y.,  
Komiyama, S. and Yoshimura, A.

A new protein containing an SH2 domain that inhibits JAK kinases  
Nature 387 (6636), 921-924 (1997)

## JOURNAL

## MEDLINE

97345634 Location/Qualifiers  
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/translation="CPAEPRRRPPSSSSSSPPAAPAPPCAPAPAPDPTFTF  
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QELCRQIVATVGENAKRIPLVNLYLDYLSSEFQI"

## CDS

BASE COUNT 161 a 358 c 285 g 224 t 2 others  
ORIGIN

## alignment\_scores:

Quality: 991.50 Length: 196  
Ratio: 5.111 Gaps: 1  
Percent Similarity: 98.980 Percent Identity: 96.429

alignment\_block:  
US-08-962-560a-4 x AB000676 ..

Align seg 1/1 to: AB000676 from: 1 to: 1030

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33 rProAlaAlaProValArgProArgProCysProAlaValProAlaPro 50
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54 GCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 103
50 lAProGlyAspThrHisPheArgThrPheArgSerHisSerAspTyrArg 66
|||||...|||||
104 CCGCGCGCGCAGCAGCACTTCGCGCATTCGCTGCGACCGCATTAACGG 153
67 ArgIleThrArgThrSerAlaLeuAspAlaCysGlyPheTyrTrp 83
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154 CGCATCAGCGCGCCAGCGCGCTCTGACGCGCTGGGATTTCTACTGGGG 203
83 yProLeuSerValHisGlyAlaHisGluArgLeuArgAlaGluProValG 100
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204 GCCCTGACGCTGACAGGGGCGCACAGCGCGCTGGCGCGCGAGCCGCTGG 253
100 lYThrPheLeuValArgAspSerArgGlnArgAsnCysPheAlaLeu 116
|||||
254 GCACCTTCTCTGGTGGCGCACAGCGCGCGAGACTGCTTTTCGCCCTT 303
117 SerValLysMetAlaSerGlyProThrSerIleArgValHisPheGlnAl 133
|||||
304 AGCGTGAAGATGGCTCGGAGCCACAGAGCATCCGGTGCTGACTTCAGGC 353
133 acIlyArgPheHisLeuAspGlySerArgGluThrPheAspCysLeuPheG 150
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354 CGCGCGCTTTCACCTGGATGGCAGCGCGAGCTTCGACTGCTCTTGG 403
150 luleuLeuGluHisIleValAlaAlaProArgArgMetLeuGlyAlaPro 166
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404 AGCTGCTGAGCACAACGTCGTGGCGCGCGCGCGCATGCTGGGGGCCCG 453
167 leuArgGlnArgValArgProLeuGlnGluLeuCysArgGlnArgTl 183
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454 CTGGCCAGCGCGCGCGCTGGCGCGCTGCAAGAGCTGTGCCCGCAGGCGCAT 503
183 eValAlaAlaValGlyArgGluAsnLeuAlaArgIleProLeuAsnProy 200
|||||
504 CGTGGCCACCGTGGGCGCGAGAACCTGGCTGCAATCCCTCAACCCCG 553
200 alleuArgAspTyrLeuSerSerPheProPheGlnIle 212
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554 TCCTCGCGCAGTACCTGAGCTCTCTCCCTTCAGATT 591
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